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C

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANTS: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA GRODEN
- (ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME
- (iii) NUMBER OF SEQUENCES: 78
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
 - (B) STREET: 90 PARK AVENUE
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10016
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: MS-DOS
 - (D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/559,303
 - (B) FILING DATE: NOVEMBER 15, 1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: ELIZABETH A. BOGOSIAN
 - (B) REGISTRATION NUMBER: 39,911
 - (C) REFERENCE/DOCKET NUMBER: 63475/65
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 697-5995
 - (B) TELEFAX: (212) 286-0854 or 286-0082
 - (C) TELEX: TWX 710-581-4766

(2) INFORMATION FOR SEQ ID NO: 1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

GGTGGCGACG ACTCCTGGA 19

(3) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

ACCAGACCAA CTGGTAATG 19

(4) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

ATGGTAGCGA CCGGCGCTCA 20

(5) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

CCGTCAGTAT CCGCGGAATT 20

(6) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

TTGTGGTGTT GGCTAGAGGT T 21

(7) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

GCCGCCGGCA CCAAC 15

(8) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

CCTCAGTCAA ATCTATNTGC TC 22

(9) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

GCCATCACCG GAACAGAAGG AAA 23

(10) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

TCTTCTGGAG GAGGTGGAAC AA 22

(11) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

GGATCCTGGT TCCGTCCGC 19

(12) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

CAACTAGAAC GTCACTCAGC C 21

(13) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

GACITTTTCCT TCAGTGAACC TC 22

(14) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13
CCAGATTCT TGCAGACTCC G 21

(15) INFORMATION FOR SEQ ID NO: 14

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14
CTTTAAGTAC CATCAATGAT TGGG 24

(16) INFORMATION FOR SEQ ID NO: 15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:

- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

GAGTAAGCAC TGCTCAGAAA TC 22

(17) INFORMATION FOR SEQ ID NO: 16

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

CGAGCAAATA GATTGACTG AGG 23

(18) INFORMATION FOR SEQ ID NO: 17

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:

- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

GAAGATGCTC AGGAAAGTGA C 21

(19) INFORMATION FOR SEQ ID NO: 18

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

CAACTGAGAA AGTTCCATGT ATTG 24

(20) INFORMATION FOR SEQ ID NO: 19

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CTATTCCTGA TGATAAACTG AAAC 24

(21) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

GTGGAGATAC AGGCCTGATT C 21

(22) INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

CAGGATTCTC TGCCACCAGG 20

(23) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

CAGGAAATGT TCTACAAGC AC 22

(24) INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

CAGCCAGCAA ATCTTCCACA G 21

(25) INFORMATION FOR SEQ ID NO: 24

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24
GAATTATACT GACAAGTCAG CAC 23

(26) INFORMATION FOR SEQ ID NO: 25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CTCCTGGGGT CACTGTTGTC 20

(27) INFORMATION FOR SEQ ID NO: 26

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

GAGGTTCACT GAAGGAAAAG TC 22

(28) INFORMATION FOR SEQ ID NO: 27

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

GAAGTCCTTG ACCCTTTGCT G 21

(29) INFORMATION FOR SEQ ID NO: 28

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28
GGGATTCTT TACAGTTGGT GTG 23

(30) INFORMATION FOR SEQ ID NO: 29

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29
CTCTTACAAA GTGACTTTGG GG 22

(31) INFORMATION FOR SEQ ID NO: 30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30
CCTCAGTCAA ATCTATTTGC TCG 23

(32) INFORMATION FOR SEQ ID NO: 31

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31
GCTTAACCAT TCTGAGTCAT CC 22

(33) INFORMATION FOR SEQ ID NO: 32

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32
CAATACATGG AACTTTCTCA GTTG 24

(34) INFORMATION FOR SEQ ID NO: 33

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33
CGTACTAAGG CATTTTGAAG AGG 23

(35) INFORMATION FOR SEQ ID NO: 34

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34
CACAGTCTGT GCTGGTTTCT G 21

(36) INFORMATION FOR SEQ ID NO: 35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35
CCTTCATAGA ATTCCCTGTA GG 22

(37) INFORMATION FOR SEQ ID NO: 36

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36
GTGTTTCAGC CCAGTTGCTA C 21

(38) INFORMATION FOR SEQ ID NO: 37

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37
GCAGTATGTT TATTCTGATC TTTC 24

(39) INFORMATION FOR SEQ ID NO: 38

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38
CCTTGATGGG TTGATAGGCA G 21

(40) INFORMATION FOR SEQ ID NO: 39

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39
CGCTCATGTT TCAGATTCT GG 22

(41) INFORMATION FOR SEQ ID NO: 40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40
GATCTACGAT AAGTGATCTC AAG 23

(42) INFORMATION FOR SEQ ID NO: 41

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41
GAGTCTGTTA CTTGCACAGA TC 22

(43) INFORMATION FOR SEQ ID NO: 42

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42
CAATCATAAA ACTTCTATAT GTCAC 25

(44) INFORMATION FOR SEQ ID NO: 43

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43
GTGGGGACAT GATTTTCGTC AAG 23

(45) INFORMATION FOR SEQ ID NO: 44

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44
GACATCCTGA CTCAGCTGAA G 21

(46) INFORMATION FOR SEQ ID NO: 45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45
GCACCACCCA TATGATTCAG G 21

(47) INFORMATION FOR SEQ ID NO: 46

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46
GATGAAGTGC AGCAGAAGTG G 21

(48) INFORMATION FOR SEQ ID NO: 47

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47
GCAGAGCTGG AAGAGATGGG 20

(49) INFORMATION FOR SEQ ID NO: 48

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48
GTATAGCATG GTACATTACT GTG 23

(50) INFORMATION FOR SEQ ID NO: 49

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49
GACTGACGAT GTGAAAAGTA TTG 23

(51) INFORMATION FOR SEQ ID NO: 50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50
CCAGTCAGGT ATATTGGA AAG 23

(52) INFORMATION FOR SEQ ID NO: 51

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51
CGATCGCTTA TGTGATGCTC G 21

(53) INFORMATION FOR SEQ ID NO: 52

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52
GAACTTACAG AAGTCTGCAA ATC 23

(54) INFORMATION FOR SEQ ID NO: 53

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53
GGTGTTACTG AAGACAAACT GG 22

(55) INFORMATION FOR SEQ ID NO: 54

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54
GGATAAGCCT GTCCAGCAGC 20

(56) INFORMATION FOR SEQ ID NO: 55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55
GCTTCCAGTG GTTCCAAGGC 20

(57) INFORMATION FOR SEQ ID NO: 56

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56
CTCAAGCGAC ATCAGGAGCC 20

(58) INFORMATION FOR SEQ ID NO: 57

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57
GCCATCACCG GAACAGAAGG 20

(59) INFORMATION FOR SEQ ID NO: 58

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58
GATTATGTCT GTTAAAGCTC ATG 23

(60) INFORMATION FOR SEQ ID NO: 59

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59
CGTGTCAGCC ATGGTGTCAC 20

(61) INFORMATION FOR SEQ ID NO: 60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60
CAGATAACCT GACAGCCATC C 21

(62) INFORMATION FOR SEQ ID NO: 61

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61
CAGTCTGGTC ACATCATGAT AG 22

(63) INFORMATION FOR SEQ ID NO: 62

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62
GCTGTATTCT CCTGCATTCC G 21

(64) INFORMATION FOR SEQ ID NO: 63

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63
CCTTGTGATG AACTATGTTC TTG 23

(65) INFORMATION FOR SEQ ID NO: 64

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64
CCAAAATCTT GTCAAGTATC AGC 23

(66) INFORMATION FOR SEQ ID NO: 65

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65
GGAATTTTCT GTTTCATAA AGTC 24

(67) INFORMATION FOR SEQ ID NO: 66

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66
CAAGCTTCTT GAGAGTGACG G 21

(68) INFORMATION FOR SEQ ID NO: 67

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67
GATGTCCATT CAGAGTATTT CTG 23

(69) INFORMATION FOR SEQ ID NO: 68

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68
GGGTATTTCC TCGTCAAGCT C 21

(70) INFORMATION FOR SEQ ID NO: 69

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69
CCTAGATATC TTTCTACATG TGG 23

(71) INFORMATION FOR SEQ ID NO: 70

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70
GTTATGAGAA TGCATATGAA GGC 23

(72) INFORMATION FOR SEQ ID NO: 71

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71
CAAGAATAAC AGCTTTATAG TCAC 24

(73) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4437
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

GCGCGGCGGC CGTGGTTGCG GCGCGGGAAG TTTGGATCCT GGTTCGGTCC GCTAGGAGTC	60
TGCGTGCGAG GATTATGGCT GCTGTTCTC AAAATAATCT ACAGGAGCAA CTAGAACGTC	120
ACTCAGCCAG AACACTTAAT AATAAATTAA GTCTTTCAAA ACCAAAATTT TCAGGTTTCA	180
CTTTTAAAAA GAAAACATCT TCAGATAACA ATGTATCTGT AACTAATGTG TCAGTAGCAA	240
AAACACCTGT ATTAAGAAAT AAAGATGTTA ATGTTACCGA AGACTTTTCC TTCAGTGAAC	300
CTCTACCCAA CACCACAAAT CAGCAAAGGG TCAAGGACTT CTTTAAAAAT GCTCCAGCAG	360
GACAGGAAAC ACAGAGAGGT GGATCAAAAT CATTATTGCC AGATTTCTTG CAGACTCCGA	420
AGGAAGTTGT ATGCACTACC CAAAACACAC CAACTGTAAA GAAATCCCGG GATACTGCTC	480
TCAAGAAATT AGAATTTAGT TCTTCACCAG ATTCTTTAAG TACCATCAAT GATTGGGATG	540
ATATGGATGA CTTTGATACT TCTGAGACTT CAAAATCATT TGTTACACCA CCCCAAAGTC	600
ACTTTGTAAG AGTAAGCACT GCTCAGAAAT CAAAAAAGGG TAAGAGAAAC TTTTTTAAAG	660
CACAGCTTTA TACAACAAAC ACAGTAAAGA CTGATTTGCC TCCACCCTCC TCTGAAAGCG	720
AGCAAATAGA TTTGACTGAG GAACAGAAGG ATGACTCAGA ATGGTTAAGC AGCGATGTGA	780
TTTGCATCGA TGATGGCCCC ATTGCTGAAG TGCATATAAA TGAAGATGCT CAGGAAAGTG	840
ACTCTCTGAA AACTCATTTG GAAGATGAAA GAGATAATAG CGAAAAGAAG AAGAATTTGG	900

AAGAAGCTGA ATTACATTCA ACTGAGAAAG TTCCATGTAT TGAATTTGAT GATGATGATT 960
ATGATACGGA TTTTGTTCCTA CCTTCTCCAG AAGAAATTAT TTCTGCTTCT TCTTCCTCTT 1020
CAAAATGCCT TACTACGTTA AAGGACCTTG ACACATCTGA CAGAAAAGAG GATGTTCTTA 1080
GCACATCAAA AGATCTTTTG TCAAAACCTG AGAAAATGAG TATGCAGGAG CTGAATCCAG 1140
AAACCAGCAC AGACTGTGAC GCTAGACAGA TAAGTTTACA GCAGCAGCTT ATTCATGTGA 1200
TGGAGCACAT CTGTAAATTA ATTGATACTA TTCCTGATGA TAAACTGAAA CTTTTGGATT 1260
GTGGGAACGA ACTGCTTCAG CAGCGGAACA TAAGAAGGAA ACTTCTAACG GAAGTAGATT 1320
TTAATAAAAAG TGATGCCAGT CTTCTTGGCT CATTGTGGAG ATACAGGCCT GATTCACTTG 1380
ATGGCCCTAT GGAGGGTGAT TCCTGCCCTA CAGGGAATTC TATGAAGGAG TTAAATTTTT 1440
CACACCTTCC CTCAAATTCT GTTCTCCTG GGGACTGTTT ACTGACTACC ACCCTAGGAA 1500
AGACAGGATT CTCTGCCACC AGGAAGAATC TTTTGTAAAG GCCTTTATTC AATACCCATT 1560
TACAGAAAGTC CTTTGTAAGT AGCAACTGGG CTGAAACACC AAGACTAGGA AAAAAAATG 1620
AAAGCTCTTA TTTCCCAGGA AATGTTCTCA CAAGCACTGC TGTGAAAGAT CAGAATAAAC 1680
ATACTGCTTC AATAAATGAC TTAGAAAGAG AAACCCAACC TTCCTATGAT ATTGATAATT 1740
TTGACATAGA TGACTTTGAT GATGATGATG ACTGGGAAGA CATAATGCAT AATTTAGCAG 1800
CCAGCAAATC TTCCACAGCT GCCTATCAAC CCATCAAGGA AGGTCGGCCA ATTAAATCAG 1860
TATCAGAAAG ACTTTCCTCA GCCAAGACAG ACTGTCTTCC AGTGTCTCTT ACTGCTCAAA 1920
ATATAAACTT CTCAGAGTCA ATTCAGAATT ATACTGACAA GTCAGCACAA AATTTAGCAT 1980
CCAGAAATCT GAAACATGAG CGTTTCCAAA GTCTTAGTTT TCCTCATACA AAGGAAATGA 2040
TGAAGATTTT TCATAAAAAA TTTGGCCTGC ATAATTTTAG AACTAATCAG CTAGAGGCGA 2100
TCAATGCTGC ACTGCTTGGT GAAGACTGTT TTATCCTGAT GCCGACTGGA GGTGGTAAGA 2160
GTTTGTGTTA CCAGCTCCCT GCCTGTGTTT CTCCTGGGGT CACTGTTGTC ATTTCTCCCT 2220
TGAGATCACT TATCGTAGAT CAAGTCCAAA AGCTGACTTC CTTGGATATT CCAGCTACAT 2280
ATCTGACAGG TGATAAGACT GACTCAGAAG CTACAAATAT TTACCTCCAG TTATCAAAAA 2340
AAGACCCAAT CATAAACTT CTATATGTCA CTCCAGAAAA GATCTGTGCA AGTAACAGAC 2400
TCATTTCTAC TCTGGAGAAT CTCTATGAGA GGAAGCTCTT GGCACGTTTT GTTATTGATG 2460

AAGCACATTG TGTCAGTCAG TGGGGACATG ATTTTCGTCA AGATTACAAA AGAATGAATA 2520
TGCTTCGCCA GAAGTTTCCT TCTGTTCCGG TGATGGCTCT TACGGCCACA GCTAATCCCA 2580
GGGTACAGAA GGACATCCTG ACTCAGCTGA AGATTCTCAG ACCTCAGGTG TTTAGCATGA 2640
GCTTTAACAG ACATAATCTG AAATACTATG TATTACCGAA AAAGCCTAAA AAGGTGGCAT 2700
TTGATTGCCT AGAATGGATC AGAAAGCACC ACCCATATGA TTCAGGGATA ATTTACTGCC 2760
TCTCCAGGCG AGAATGTGAC ACCATGGCTG ACACGTTACA GAGAGATGGG CTCGCTGCTC 2820
TTGCTTACCA TGCTGGCCTC AGTGATTCTG CCAGAGATGA AGTGCAGCAG AAGTGGATTA 2880
ATCAGGATGG CTGTCAGGTT ATCTGTGCTA CAATTGCATT TGAATGGGG ATTGACAAAC 2940
CGGACGTGCG ATTTGTGATT CATGCATCTC TCCCTAAATC TGTGGAGGGT TACTACCAAG 3000
AATCTGGCAG AGCTGGAAGA GATGGGGAAA TATCTCACTG CCTGCTTTTC TATACCTATC 3060
ATGATGTGAC CAGACTGAAA AGACTTATAA TGATGGAAA AGATGGAAAC CATCATACAA 3120
GAGAAACTCA CTTCAATAAT TTGTATAGCA TGGTACATTA CTGTGAAAAT ATAACGGAAT 3180
GCAGGAGAAT ACAGCTTTTG GCCTACTTTG GTGAAAATGG ATTTAATCCT GATTTTTGTA 3240
AGAAACACCC AGATGTTTCT TGTGATAATT GCTGTAAAC AAAGGATTAT AAAACAAGAG 3300
ATGTGACTGA CGATGTGAAA AGTATTGTAA GATTTGTTCA AGAACATAGT TCATCACAAG 3360
GAATGAGAAA TATAAAACAT GTAGGTCCTT CTGGAAGATT TACTATGAAT ATGCTGGTCG 3420
ACATTTTCTT GGGGAGTAAG AGTGCAAAAA TCCAGTCAGG TATATTGGA AAAGGATCTG 3480
CTTATTCACG ACACAATGCC GAAAGACTTT TTAAAAAGCT GATACTTGAC AAGATTTTGG 3540
ATGAAGACTT ATATATCAAT GCCAATGACC AGGCGATCGC TTATGTGATG CTCGGAAATA 3600
AAGCCCAAAC TGTACTAAAT GGCAATTAA AGGTAGACTT TATGGAAACA GAAAATTCCA 3660
GCAGTGTGAA AAAACAAAAA GCGTTAGTAG CAAAAGTGTC TCAGAGGGAA GAGATGGTTA 3720
AAAAATGTCT TGGAGAACTT ACAGAAGTCT GCAAATCTCT GGGGAAAGTT TTTGGTGTCC 3780
ATTACTTCAA TATTTTAAAT ACCGTCCTC TCAAGAAGCT TGCAGAATCT TTATCTTCTG 3840
ATCCTGAGGT TTTGCTTCAA ATTGATGGTG TTAAGAAGA CAACTGGAA AAATATGGTG 3900
CGGAAGTGAT TTCAGTATTA CAGAAATACT CTGAATGGAC ATCGCCAGCT GAAGACAGTT 3960
CCCCAGGGAT AAGCCTGTCC AGCAGCAGAG GCCCCGGAAG AAGTGCCGCT GAGGAGCTTG 4020

ACGAGGAAAT ACCCGTATCT TCCCACTACT TTGCAAGTAA AACCAGAAAT GAAAGGAAGA 4080
GGAAAAAGAT GCCAGCCTCC CAAAGGTCTA AGAGGAGAAA AACTGCTTCC AGTGGTTCCA 4140
AGGCAAAGGG GGGGTCTGCC ACATGTAGAA AGATATCTTC CAAAACGAAA TCCTCCAGCA 4200
TCATTGGATC CAGTTCAGCC TCACATACTT CTCAAGCGAC ATCAGGAGCC AATAGCAAAT 4260
TGGGGATTAT GGCTCCACCG AAGCCTATAA ATAGACCGTT TCTTAAGCCT TCATATGCAT 4320
TCTCATAACA ACCGAATCTC AATGTACATA GACCCTCTTT CTTGTTTGTC AGCATCTGAC 4380
CATCTGTGAC TATAAAGCTG TTATTCTTGT TATACCAAAA AAAAAAAAAA AAAAAA 4437

(74) INFORMATION FOR SEQ ID NO: 73

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

GCTTCCGGCG GAAGTGAGCC AGGGCTTGGC GCGGCGGCCG TGGTTGCGGC 50
GCGGGAAGTT TGGAT 65

(75) INFORMATION FOR SEQ ID NO: 74

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE:
 (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 (A) NAME/KEY:
 (B) LOCATION:
 (C) IDENTIFICATION METHOD:
 (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

Phe	Pro	His	Thr	Lys	Glu	Met	Met	Lys	Ile	Phe	His	Lys	Lys	Phe	1	5	10	15
Gly	Leu	His	Asn	Phe	Arg	Thr	Asn	Gln	Leu	Glu	Ala	Ile	Asn	Ala	20	25	30	
Ala	Leu	Leu	Gly	Glu	Asp	Cys	Phe	Ile	Leu	Met	Pro	Thr	Gly	Gly	35	40	45	
Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Leu	Pro	Ala	Cys	Val	Ser	Pro	Gly	50	55	60	
Val	Thr	Val	Val	Ile	Ser	Pro	Leu	Arg	Ser	Leu	Ile	Val	Asp	Gln	65	70	75	
Val	Gln	Lys	Leu	Thr	Ser	Leu	Asp	Ile	Pro	Ala	Thr	Tyr	Leu	Thr	80	85	90	
Gly	Asp	Lys	Thr	Asp	Ser	Glu	Ala	Thr	Asn	Ile	Tyr	Leu	Gln	Leu	95	100	105	
Ser	Lys	Lys	Asp	Pro	Ile	Ile	Lys	Leu	Leu	Tyr	Val	Thr	Pro	Glu	110	115	120	
Lys	Ile	Cys	Ala	Ser	Asn	Arg	Leu	Ile	Ser	Thr	Leu	Glu	Asn	Leu	125	130	135	
Tyr	Glu	Arg	Lys	Leu	Leu	Ala	Arg	Phe	Val	Ile	Asp	Glu	Ala	His	140	145	150	
Cys	Val	Ser	Gln	Trp	Gly	His	Asp	Phe	Arg	Gln	Asp	Tyr	Lys	Arg	155	160	165	
Met	Asn	Met	Leu	Arg	Gln	Lys	Phe	Pro	Ser	Val	Pro	Val	Met	Ala	170	175	180	

Leu Thr Ala Thr	Ala Asn Pro Arg Val	Gln Lys Asp Ile Leu Thr	
	185	190	195
Gln Leu Lys Ile	Leu Arg Pro Gln Val	Phe Ser Met Ser Phe Asn	
	200	205	210
Arg His Asn Leu	Lys Tyr Tyr Val Leu	Pro Lys Lys Pro Lys Lys	
	215	220	225
Val Ala Phe Asp	Cys Leu Glu Trp Ile	Arg Lys His His Pro Tyr	
	230	235	240
Asp Ser Gly Ile	Ile Tyr Cys Leu Ser	Arg Arg Glu Cys Asp Thr	
	245	250	255
Met Ala Asp Thr	Leu Gln Arg Asp Gly	Leu Ala Ala Leu Ala Tyr	
	260	265	270
His Ala Gly Leu	Ser Asp Ser Ala Arg	Asp Glu Val Gln Gln Lys	
	275	280	285
Trp Ile Asn Gln	Asp Gly Cys Gln Val	Ile Cys Ala Thr Ile Ala	
	290	295	300
Phe Gly Met Gly	Ile Asp Lys Pro Asp	Val Arg Phe Val Ile His	
	305	310	315
Ala Ser Leu Pro	Lys Ser Val Glu Gly	Tyr Tyr Gln Glu Ser Gly	
	320	325	330
Arg Ala Gly Arg	Asp Gly Glu Ile Ser	His Cys Leu Leu Phe Tyr	
	335	340	345
Thr Tyr His Asp	Val Thr Arg Leu Lys	Arg Leu Ile Met Met Glu	
	350	355	360
Lys Asp Gly Asn	His His Thr Arg Glu	Thr His Phe Asn Asn Leu	
	365	370	375
Tyr Ser Met Val	His Tyr Cys Glu Asn	Ile Thr Glu Cys Arg Arg	
	380	385	390
Ile Gln Leu			

(76) INFORMATION FOR SEQ ID NO: 75

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
 - (C) IDENTIFICATION METHOD:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

Phe	Pro	Trp	Ser	Gly	Lys	Val	Lys	Asp	Ile	Leu	Gln	Asn	Val	Phe	1	5	10	15
Lys	Leu	Glu	Lys	Phe	Arg	Pro	Leu	Gln	Leu	Glu	Thr	Ile	Asn	Val	20	25	30	
Thr	Met	Ala	Gly	Lys	Glu	Val	Phe	Leu	Val	Met	Pro	Thr	Gly	Gly	35	40	45	
Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Leu	Pro	Ala	Leu	Cys	Ser	Asp	Gly	50	55	60	
Phe	Thr	Leu	Val	Ile	Cys	Pro	Leu	Ile	Ser	Leu	Met	Glu	Asp	Gln	65	70	75	
Leu	Met	Val	Leu	Lys	Gln	Leu	Gly	Ile	Ser	Ala	Thr	Met	Leu	Asn	80	85	90	
Ala	Ser	Ser	Ser	Lys	Glu	His	Val	Lys	Trp	Val	His	Asp	Glu	Met	95	100	105	
Val	Asn	Lys	Asn	Ser	Glu	Leu	Lys	Leu	Ile	Tyr	Val	Thr	Pro	Glu	110	115	120	
Lys	Ile	Ala	Lys	Ser	Lys	Met	Phe	Met	Ser	Arg	Leu	Glu	Lys	Ala	125	130	135	
Tyr	Glu	Ala	Arg	Arg	Phe	Thr	Arg	Ile	Ala	Val	Asp	Glu	Val	His	140	145	150	
Cys	Cys	Ser	Gln	Trp	Gly	His	Asp	Phe	Arg	Pro	Asp	Tyr	Lys	Ala	155	160	165	
Leu	Gly	Ile	Leu	Lys	Arg	Gln	Phe	Pro	Asn	Ala	Ser	Leu	Ile	Gly	170	175	180	

Leu Thr Ala Thr	Ala Thr Asn His Val	Leu Thr Asp Ala Gln Lys
185		190 195
Ile Leu Cys Ile	Glu Lys Cys Phe Thr	Phe Thr Ala Ser Phe Asn
200		205 210
Arg Pro Asn Leu	Tyr Tyr Glu Val Arg	Gln Lys Pro Ser Asn Thr
215		220 225
Glu Asp Phe Ile	Glu Asp Ile Val Lys	Leu Ile Asn Gly Arg Tyr
230		235 240
Lys Gly Gln Ser	Gly Ile Ile Tyr Cys	Phe Ser Gln Lys Asp Ser
245		250 255
Glu Gln Val Thr	Val Ser Leu Gln Asn	Leu Gly Ile His Ala Gly
260		265 270
Ala Tyr His Ala	Asn Leu Glu Pro Glu	Asp Lys Thr Thr Val His
275		280 285
Arg Lys Trp Ser	Ala Asn Glu Ile Gln	Val Val Val Ala Thr Val
290		295 300
Ala Phe Gly Met	Gly Ile Asp Lys Pro	Asp Val Arg Phe Val Ile
305		310 315
His His Ser Met	Ser Lys Ser Met Glu	Asn Tyr Tyr Gln Glu Ser
320		325 330
Gly Arg Ala Gly	Arg Asp Asp Met Lys	Ala Asp Cys Ile Leu Tyr
335		340 345
Tyr Gly Phe Gly	Asp Ile Phe Arg Ile	Ser Ser Met Val Val Met
350		355 360
Glu Asn Val Gly	Gln Gln Lys Leu Tyr	Glu Met Val Ser Tyr Cys
365		370 375
Gln Asn Ile Ser	Lys Ser Arg Arg Val	Leu Met
380		385

(77) INFORMATION FOR SEQ ID NO: 76.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

Tyr	Pro	Trp	Ser	Asp	Glu	Val	Leu	Tyr	Arg	Leu	His	Glu	Val	Phe	1	5	10	15
Lys	Leu	Pro	Gly	Phe	Arg	Pro	Asn	Gln	Leu	Glu	Ala	Val	Asn	Ala	20	25	30	
Thr	Leu	Gln	Gly	Lys	Asp	Val	Phe	Val	Leu	Met	Pro	Thr	Gly	Gly	35	40	45	
Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Leu	Pro	Ala	Val	Val	Lys	Ser	Gly	50	55	60	
Lys	Thr	His	Gly	Thr	Thr	Ile	Val	Ile	Ser	Pro	Leu	Ile	Ser	Leu	65	70	75	
Met	Gln	Asp	Gln	Val	Glu	His	Leu	Leu	Asn	Lys	Asn	Ile	Lys	Ala	80	85	90	
Ser	Met	Phe	Ser	Ser	Arg	Gly	Thr	Ala	Glu	Gln	Arg	Arg	Gln	Thr	95	100	105	
Phe	Asn	Leu	Phe	Ile	Asn	Gly	Leu	Leu	Asp	Leu	Val	Tyr	Ile	Ser	110	115	120	
Pro	Glu	Met	Ile	Ser	Ala	Ser	Glu	Gln	Cys	Lys	Arg	Ala	Ile	Ser	125	130	135	
Arg	Leu	Tyr	Ala	Asp	Gly	Lys	Leu	Ala	Arg	Ile	Val	Val	Asp	Glu	140	145	150	
Ala	His	Cys	Val	Ser	Asn	Trp	Gly	His	Asp	Phe	Arg	Pro	Asp	Tyr	155	160	165	
Lys	Glu	Leu	Lys	Phe	Phe	Lys	Arg	Glu	Tyr	Pro	Asp	Ile	Pro	Met	170	175	180	
Ile	Ala	Leu	Thr	Ala	Thr	Ala	Ser	Glu	Gln	Val	Arg	Met	Asp	Ile	185	190	195	

Ile	His	Asn	Leu	Glu	Leu	Lys	Glu	Pro	Val	Phe	Leu	Lys	Gln	Ser	200	205	210
Phe	Asn	Arg	Thr	Asn	Leu	Tyr	Tyr	Glu	Val	Asn	Lys	Lys	Thr	Lys	215	220	225
Asn	Thr	Ile	Phe	Glu	Ile	Cys	Asp	Ala	Val	Lys	Ser	Arg	Phe	Lys	230	235	240
Asn	Gln	Thr	Gly	Ile	Ile	Tyr	Cys	His	Ser	Lys	Lys	Ser	Cys	Glu	245	250	255
Gln	Thr	Ser	Ala	Gln	Met	Gln	Arg	Asn	Gly	Ile	Lys	Cys	Ala	Tyr	260	265	270
Tyr	His	Ala	Gly	Met	Glu	Pro	Asp	Glu	Arg	Leu	Ser	Val	Gln	Lys	275	280	285
Ala	Trp	Gln	Ala	Asp	Glu	Ile	Gln	Val	Ile	Cys	Ala	Thr	Val	Ala	290	295	300
Phe	Gly	Met	Gly	Ile	Asp	Lys	Pro	Asp	Val	Arg	Phe	Val	Tyr	His	305	310	315
Phe	Thr	Val	Pro	Arg	Thr	Leu	Glu	Gly	Tyr	Tyr	Gln	Glu	Thr	Gly	320	325	330
Arg	Ala	Gly	Arg	Asp	Gly	Asp	Tyr	Ser	Tyr	Cys	Ile	Thr	Tyr	Phe	335	340	345
Ser	Phe	Arg	Asp	Ile	Arg	Thr	Met	Gln	Thr	Met	Ile	Gln	Lys	Asp	350	355	360
Lys	Asn	Leu	Asp	Arg	Glu	Asn	Lys	Glu	Lys	His	Leu	Asn	Lys	Leu	365	370	375
Gln	Gln	Val	Met	Ala	Tyr	Cys	Asp	Asn	Val	Thr	Asp	Cys	Arg	Arg	380	385	390

Lys Leu Val

(78) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

Val	Leu	Gln	Glu	Thr	Phe	Gly	Tyr	Gln	Gln	Phe	Arg	Pro	Gly	Gln	1	5	10	15
Glu	Glu	Ile	Ile	Asp	Thr	Val	Leu	Ser	Gly	Arg	Asp	Cys	Leu	Val	20	25	30	
Val	Met	Pro	Thr	Gly	Gly	Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Ile	Pro	35	40	45	
Ala	Leu	Leu	Leu	Asn	Gly	Leu	Thr	Val	Val	Val	Ser	Pro	Leu	Ile	50	55	60	
Ser	Leu	Met	Lys	Asp	Gln	Val	Asp	Gln	Leu	Gln	Ala	Asn	Gly	Val	65	70	75	
Ala	Ala	Ala	Cys	Leu	Asn	Ser	Thr	Gln	Thr	Arg	Glu	Gln	Gln	Leu	80	85	90	
Glu	Val	Met	Thr	Gly	Cys	Arg	Thr	Gly	Gln	Ile	Arg	Leu	Leu	Tyr	95	100	105	
Ile	Ala	Pro	Glu	Arg	Leu	Met	Leu	Asp	Asn	Phe	Leu	Glu	His	Leu	110	115	120	
Ala	His	Trp	Asn	Pro	Val	Leu	Leu	Ala	Val	Asp	Glu	Ala	His	Cys	125	130	135	
Ile	Ser	Gln	Trp	Gly	His	Asp	Phe	Arg	Pro	Glu	Tyr	Ala	Ala	Leu	140	145	150	
Gly	Gln	Leu	Arg	Gln	Arg	Phe	Pro	Thr	Leu	Pro	Phe	Met	Ala	Leu	155	160	165	
Thr	Ala	Thr	Ala	Asp	Asp	Thr	Thr	Arg	Gln	Asp	Ile	Val	Arg	Leu	170	175	180	
Leu	Gly	Leu	Asn	Asp	Pro	Leu	Ile	Gln	Ile	Ser	Ser	Phe	Asp	Arg	185	190	195	
Pro	Asn	Ile	Arg	Tyr	Met	Leu	Met	Glu	Lys	Phe	Lys	Pro	Leu	Asp				

200										205					210				
Gln	Leu	Met	Arg	Tyr	Val	Gln	Glu	Gln	Arg	Gly	Lys	Ser	Gly	Ile					
				215					220					225					
Ile	Tyr	Cys	Asn	Ser	Arg	Ala	Lys	Val	Glu	Asp	Thr	Ala	Ala	Ala					
				230					235					240					
Leu	Gln	Ser	Lys	Gly	Ile	Ser	Ala	Ala	Ala	Tyr	His	Ala	Gly	Leu					
				245					250					255					
Glu	Asn	Asn	Val	Arg	Ala	Asp	Val	Gln	Glu	Lys	Phe	Gln	Arg	Asp					
				260					265					270					
Asp	Leu	Gln	Ile	Val	Val	Ala	Thr	Val	Ala	Phe	Gly	Met	Gly	Ile					
				275					280					285					
Asn	Lys	Pro	Asn	Val	Arg	Phe	Val	Val	His	Phe	Asp	Ile	Pro	Arg					
				290					295					300					
Asn	Ile	Glu	Ser	Tyr	Tyr	Gln	Glu	Thr	Gly	Arg	Ala	Gly	Arg	Asp					
				305					310					315					
Gly	Leu	Pro	Ala	Glu	Ala	Met	Leu	Phe	Tyr	Asp	Pro	Ala	Asp	Met					
				320					325					330					
Ala	Trp	Leu	Arg	Arg	Cys	Leu	Glu	Glu	Lys	Pro	Gln	Gly	Gln	Leu					
				335					340					345					
Gln	Asp	Ile	Glu	Arg	His	Lys	Leu	Asn	Ala	Met	Gly	Ala	Phe	Ala					
				350					355					360					
Glu	Ala	Gln	Thr	Cys	Arg	Arg	Leu	Val	Leu										
				365					370										

(79) INFORMATION FOR SEQ ID NO: 78

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1417
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:

				Met 1	Ala	Ala	Val	Pro 5	Gln	Asn	Asn	Leu	Gln 10	Glu	Gln
Leu	Glu	Arg 15	His	Ser	Ala	Arg	Thr 20	Leu	Asn	Asn	Lys	Leu 25	Ser	Leu	Ser
Lys	Pro 30	Lys	Phe	Ser	Gly	Phe 35	Thr	Phe	Lys	Lys	Lys 40	Thr	Ser	Ser	Asp
Asn 45	Asn	Val	Ser	Val	Thr 50	Asn	Val	Ser	Val	Ala 55	Lys	Thr	Pro	Val	Leu 60
Arg	Asn	Lys	Asp	Val 65	Asn	Val	Thr	Glu	Asp 70	Phe	Ser	Phe	Ser	Glu 75	Pro
Leu	Pro	Asn	Thr 80	Thr	Asn	Gln	Gln	Arg 85	Val	Lys	Asp	Phe	Phe 90	Lys	Asn
Ala	Pro	Ala 95	Gly	Gln	Glu	Thr	Gln 100	Arg	Gly	Gly	Ser	Lys 105	Ser	Leu	Leu
Pro	Asp 110	Phe	Leu	Gln	Thr	Pro 115	Lys	Glu	Val	Val	Cys 120	Thr	Thr	Gln	Asn
Thr 125	Pro	Thr	Val	Lys	Lys 130	Ser	Arg	Asp	Thr	Ala 135	Leu	Lys	Lys	Leu	Glu 140
Phe	Ser	Ser	Ser	Pro 145	Asp	Ser	Leu	Ser	Thr 150	Ile	Asn	Asp	Trp	Asp 155	Asp
Met	Asp	Asp	Phe 160	Asp	Thr	Ser	Glu	Thr 165	Ser	Lys	Ser	Phe	Val 170	Thr	Pro
Pro	Gln	Ser 175	His	Phe	Val	Arg	Val 180	Ser	Thr	Ala	Gln	Lys 185	Ser	Lys	Lys
Gly	Lys 190	Arg	Asn	Phe	Phe	Lys 195	Ala	Gln	Leu	Tyr	Thr 200	Thr	Asn	Thr	Val
Lys 205	Thr	Asp	Leu	Pro	Pro 210	Pro	Ser	Ser	Glu	Ser 215	Glu	Gln	Ile	Asp	Leu 220

Thr Glu Glu Gln Lys Asp Asp Ser Glu Trp Leu Ser Ser Asp Val Ile
225 230 235

Cys Ile Asp Asp Gly Pro Ile Ala Glu Val His Ile Asn Glu Asp Ala
240 245 250

Gln Glu Ser Asp Ser Leu Lys Thr His Leu Glu Asp Glu Arg Asp Asn
255 260 265

Ser Glu Lys Lys Lys Asn Leu Glu Glu Ala Glu Leu His Ser Thr Glu
270 275 280

Lys Val Pro Cys Ile Glu Phe Asp Asp Asp Asp Tyr Asp Thr Asp Phe
285 290 295 300

Val Pro Pro Ser Pro Glu Glu Ile Ile Ser Ala Ser Ser Ser Ser Ser
305 310 315

Lys Cys Leu Ser Thr Leu Lys Asp Leu Asp Thr Ser Asp Arg Lys Glu
320 325 330

Asp Val Leu Ser Thr Ser Lys Asp Leu Leu Ser Lys Pro Glu Lys Met
335 340 345

Ser Met Gln Glu Leu Asn Pro Glu Thr Ser Thr Asp Cys Asp Ala Arg
350 355 360

Gln Ile Ser Leu Gln Gln Gln Leu Ile His Val Met Glu His Ile Cys
365 370 375 380

Lys Leu Ile Asp Thr Ile Pro Asp Asp Lys Leu Lys Leu Leu Asp Cys
385 390 395

Gly Asn Glu Leu Leu Gln Gln Arg Asn Ile Arg Arg Lys Leu Leu Thr
400 405 410

Glu Val Asp Phe Asn Lys Ser Asp Ala Ser Leu Leu Gly Ser Leu Trp
415 420 425

Arg Tyr Arg Pro Asp Ser Leu Asp Gly Pro Met Glu Gly Asp Ser Cys
430 435 440

Pro Thr Gly Asn Ser Met Lys Glu Leu Asn Phe Ser His Leu Pro Ser
445 450 455 460

Asn Ser Val Ser Pro Gly Asp Cys Leu Leu Thr Thr Thr Leu Gly Lys
465 470 475

Thr Gly Phe Ser Ala Thr Arg Lys Asn Leu Phe Glu Arg Pro Leu Phe
480 485 490

Asn Thr His Leu Gln Lys Ser Phe Val Ser Ser Asn Trp Ala Glu Thr

495	500	505
Pro Arg Leu Gly Lys Lys Asn Glu Ser Ser Tyr Phe Pro Gly Asn Val 510 515 520		
Leu Thr Ser Thr Ala Val Lys Asp Gln Asn Lys His Thr Ala Ser Ile 525 530 535 540		
Asn Asp Leu Glu Arg Glu Thr Gln Pro Ser Tyr Asp Ile Asp Asn Phe 545 550 555		
Asp Ile Asp Asp Phe Asp Asp Asp Asp Asp Trp Glu Asp Ile Met His 560 565 570		
Asn Leu Ala Ala Ser Lys Ser Ser Thr Ala Ala Tyr Gln Pro Ile Lys 575 580 585		
Glu Gly Arg Pro Ile Lys Ser Val Ser Glu Arg Leu Ser Ser Ala Lys 590 595 600		
Thr Asp Cys Leu Pro Val Ser Ser Thr Ala Gln Asn Ile Asn Phe Ser 605 610 615 620		
Glu Ser Ile Gln Asn Tyr Thr Asp Lys Ser Ala Gln Asn Leu Ala Ser 625 630 635		
Arg Asn Leu Lys His Glu Arg Phe Gln Ser Leu Ser Phe Pro His Thr 640 645 650		
Lys Glu Met Met Lys Ile Phe His Lys Lys Phe Gly Leu His Asn Phe 655 660 665		
Arg Thr Asn Gln Leu Glu Ala Ile Asn Ala Ala Leu Leu Gly Glu Asp 670 675 680		
Cys Phe Ile Leu Met Pro Thr Gly Gly Gly Lys Ser Leu Cys Tyr Gln 685 690 695 700		
Leu Pro Ala Cys Val Ser Pro Gly Val Thr Val Val Ile Ser Pro Leu 705 710 715		
Arg Ser Leu Ile Val Asp Gln Val Gln Lys Leu Thr Ser Leu Asp Ile 720 725 730		
Pro Ala Thr Tyr Leu Thr Gly Asp Lys Thr Asp Ser Glu Ala Thr Asn 735 740 745		
Ile Tyr Leu Gln Leu Ser Lys Lys Asp Pro Ile Ile Lys Leu Leu Tyr 750 755 760		
Val Thr Pro Glu Lys Ile Cys Ala Ser Asn Arg Leu Ile Ser Thr Leu 765 770 775 780		

Glu	Asn	Leu	Tyr	Glu	Arg	Lys	Leu	Leu	Ala	Arg	Phe	Val	Ile	Asp	Glu	
				785					790					795		
Ala	His	Cys	Val	Ser	Gln	Trp	Gly	His	Asp	Phe	Arg	Gln	Asp	Tyr	Lys	
			800					805					810			
Arg	Met	Asn	Met	Leu	Arg	Gln	Lys	Phe	Pro	Ser	Val	Pro	Val	Met	Ala	
		815					820					825				
Leu	Thr	Ala	Thr	Ala	Asn	Pro	Arg	Val	Gln	Lys	Asp	Ile	Leu	Thr	Gln	
	830					835					840					
Leu	Lys	Ile	Leu	Arg	Pro	Gln	Val	Phe	Ser	Met	Ser	Phe	Asn	Arg	His	
845					850					855					860	
Asn	Leu	Lys	Tyr	Tyr	Val	Leu	Pro	Lys	Lys	Pro	Lys	Lys	Val	Ala	Phe	
				865					870					875		
Asp	Cys	Leu	Glu	Trp	Ile	Arg	Lys	His	His	Pro	Tyr	Asp	Ser	Gly	Ile	
			880					885					890			
Ile	Tyr	Cys	Leu	Ser	Arg	Arg	Glu	Cys	Asp	Thr	Met	Ala	Asp	Thr	Leu	
		895					900					905				
Gln	Arg	Asp	Gly	Leu	Ala	Ala	Leu	Ala	Tyr	His	Ala	Gly	Leu	Ser	Asp	
	910					915					920					
Ser	Ala	Arg	Asp	Glu	Val	Gln	Gln	Lys	Trp	Ile	Asn	Gln	Asp	Gly	Cys	
925					930					935					940	
Gln	Val	Ile	Cys	Ala	Thr	Ile	Ala	Phe	Gly	Met	Gly	Ile	Asp	Lys	Pro	
				945					950					955		
Asp	Val	Arg	Phe	Val	Ile	His	Ala	Ser	Leu	Pro	Lys	Ser	Val	Glu	Gly	
			960					965					970			
Tyr	Tyr	Gln	Glu	Ser	Gly	Arg	Ala	Gly	Arg	Asp	Gly	Glu	Ile	Ser	His	
		975					980					985				
Cys	Leu	Leu	Phe	Tyr	Thr	Tyr	His	Asp	Val	Thr	Arg	Leu	Lys	Arg	Leu	
	990					995					1000					
Ile	Met	Met	Glu	Lys	Asp	Gly	Asn	His	His	Thr	Arg	Glu	Thr	His	Phe	
1005					1010					1015					1020	
Asn	Asn	Leu	Tyr	Ser	Met	Val	His	Tyr	Cys	Glu	Asn	Ile	Thr	Glu	Cys	
				1025					1030					1035		
Arg	Arg	Ile	Gln	Leu	Leu	Ala	Tyr	Phe	Gly	Glu	Asn	Gly	Phe	Asn	Pro	
			1040					1045					1050			

Asp Phe Cys Lys Lys His Pro Asp Val Ser Cys Asp Asn Cys Cys Lys
 1055 1060 1065
 Thr Lys Asp Tyr Lys Thr Arg Asp Val Thr Asp Asp Val Lys Ser Ile
 1070 1075 1080
 Val Arg Phe Val Gln Glu His Ser Ser Ser Gln Gly Met Arg Asn Ile
 1085 1090 1095 1100
 Lys His Val Gly Pro Ser Gly Arg Phe Thr Met Asn Met Leu Val Asp
 1105 1110 1115
 Ile Phe Leu Gly Ser Lys Ser Ala Lys Ile Gln Ser Gly Ile Phe Gly
 1120 1125 1130
 Lys Gly Ser Ala Tyr Ser Arg His Asn Ala Glu Arg Leu Phe Lys Lys
 1135 1140 1145
 Leu Ile Leu Asp Lys Ile Leu Asp Glu Asp Leu Tyr Ile Asn Ala Asn
 1150 1155 1160
 Asp Gln Ala Ile Ala Tyr Val Met Leu Gly Asn Lys Ala Gln Thr Val
 1165 1170 1175 1180
 Leu Asn Gly Asn Leu Lys Val Asp Phe Met Glu Thr Glu Asn Ser Ser
 1185 1190 1195
 Ser Val Lys Lys Gln Lys Ala Leu Val Ala Lys Val Ser Gln Arg Glu
 1200 1205 1210
 Glu Met Val Lys Lys Cys Leu Gly Glu Leu Thr Glu Val Cys Lys Ser
 1215 1220 1225
 Leu Gly Lys Val Phe Gly Val His Tyr Phe Asn Ile Phe Asn Thr Val
 1230 1235 1240
 Thr Leu Lys Lys Leu Ala Glu Ser Leu Ser Ser Asp Phe Glu Val Leu
 1245 1250 1255 1260
 Leu Gln Ile Asp Gly Val Thr Glu Asp Lys Leu Glu Lys Tyr Gly Ala
 1265 1270 1275
 Glu Val Ile Ser Val Leu Gln Lys Tyr Ser Glu Trp Thr Ser Pro Ala
 1280 1285 1290
 Glu Asp Ser Ser Pro Gly Ile Ser Leu Ser Ser Ser Arg Gly Pro Gly
 1295 1300 1305
 Arg Ser Ala Ala Glu Glu Leu Asp Glu Glu Ile Pro Val Ser Ser His
 1310 1315 1320

Tyr Phe Ala Ser Lys Thr Arg Asn Glu Arg Lys Arg Lys Lys Met Pro
1325 1330 1335 1340

Ala Ser Gln Arg Ser Lys Arg Arg Lys Thr Ala Ser Ser Gly Ser Lys
1345 1350 1355

Ala Lys Gly Gly Ser Ala Thr Cys Arg Lys Ile Ser Ser Lys Thr Lys
1360 1365 1370

Ser Ser Ser Ile Ile Gly Ser Ser Ser Ala Ser His Thr Ser Gln Ala
1375 1380 1385

Thr Ser Gly Ala Asn Ser Lys Leu Gly Ile Met Ala Pro Pro Lys Pro
1390 1395 1400

Ile Asn Arg Pro Phe Leu Lys Pro Ser Tyr Ala Phe Ser
1405 1410 1415